

SEQUENCE LISTING

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Katsuya, OZAKI
Katsutoshi, ARA
Shuji, KAWAI
Susumu, ITO

<120> GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE

<130> 2173-106P

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1776

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (145)..(1692)

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aaattgaagg agaggggtgct tttt atg aaa ctt cat aac cgt ata att agc 171

Met Lys Leu His Asn Arg Ile Ile Ser

1

5

gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg 219

Val Leu Leu Thr Leu Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met

10

15

20

25

acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg 267

Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met

30

35

40

cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg 315

Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg

45

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tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt	363
Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val	
60 65 70	
tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat	411
Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr	
75 80 85	
ggg gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc	459
Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr	
90 95 100 105	
gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca	507
Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr	
110 115 120	
tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat	555
Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn	
125 130 135	
cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg	603
His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val	
140 145 150	
aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa	651
Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu	
155 160 165	
gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac	699
Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn	
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ttt aaa tgg cgc tgg tat cat ttt gat ggg aca gat tgg gat cag tca	747
Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser	
190 195 200	
cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gga aag gca	795
Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala	
205 210 215	
tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg	843
Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met	
220 225 230	
tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga	891
Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg	
235 240 245	

aat	tgg	gga	gtt	tgg	tat	aca	aat	aca	ctt	aat	cta	gat	gga	ttt	aga	939
Asn	Trp	Gly	Val	Trp	Tyr	Thr	Asn	Thr	Leu	Asn	Leu	Asp	Gly	Phe	Arg	
250					255					260					265	
atc	gat	gct	gtg	aaa	cat	att	aaa	tac	agc	tat	acg	aga	gat	tgg	cta	987
Ile	Asp	Ala	Val	Lys	His	Ile	Lys	Tyr	Ser	Tyr	Thr	Arg	Asp	Trp	Leu	
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aca	cat	gtg	cgt	aac	acc	aca	ggt	aaa	cca	atg	ttt	gca	gtt	gca	gaa	1035
Thr	His	Val	Arg	Asn	Thr	Thr	Gly	Lys	Pro	Met	Phe	Ala	Val	Ala	Glu	
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ttt	tgg	aaa	aat	gac	ctt	gct	gca	atc	gaa	aac	tat	tta	aat	aaa	aca	1083
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agt	tgg	aat	cac	tcc	gtg	ttc	gat	gtt	cct	ctt	cat	tat	aat	ttg	tac	1131
Ser	Trp	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	
	315					320					325					
aat	gca	tct	aat	agt	ggt	ggc	tat	ttt	gat	atg	aga	aat	att	tta	aat	1179
Asn	Ala	Ser	Asn	Ser	Gly	Gly	Tyr	Phe	Asp	Met	Arg	Asn	Ile	Leu	Asn	
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ggt	tct	gtc	gta	caa	aaa	cac	cct	ata	cat	gca	gtc	aca	ttt	gtt	gat	1227
Gly	Ser	Val	Val	Gln	Lys	His	Pro	Ile	His	Ala	Val	Thr	Phe	Val	Asp	
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Asn	His	Asp	Ser	Gln	Pro	Gly	Glu	Ala	Leu	Glu	Ser	Phe	Val	Gln	Ser	
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Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Leu	Ile	Leu	Thr	Arg	Glu	Gln	Gly	
		380					385					390				
tac	cct	tcc	gta	ttt	tac	ggt	gat	tac	tac	ggt	ata	cca	act	cat	ggt	1371
Tyr	Pro	Ser	Val	Phe	Tyr	Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	
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gtt	cct	tcg	atg	aaa	tct	aaa	att	gat	cca	ctt	ctg	cag	gca	cgt	caa	1419
Val	Pro	Ser	Met	Lys	Ser	Lys	Ile	Asp	Pro	Leu	Leu	Gln	Ala	Arg	Gln	
410					415					420					425	
acg	tat	gcc	tac	gga	acc	caa	cat	gat	tat	ttt	gat	cat	cat	gat	att	1467
Thr	Tyr	Ala	Tyr	Gly	Thr	Gln	His	Asp	Tyr	Phe	Asp	His	His	Asp	Ile	
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atc ggc tgg acg aga gaa ggg gac agc tcc cac cca aat tca gga ctt 1515
 Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu
 445 450 455

gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc 1563
 Ala Thr Ile Met Ser Asp Gly Pro Gly Gly Asn Lys Trp Met Tyr Val
 460 465 470

ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg 1611
 Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg
 475 480 485

tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta 1659
 Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val
 490 495 500 505

aac gga ggg gca gtt tcg gtt tgg gtg aag caa taaataagga acaagaggcg 1712
 Asn Gly Gly Ala Val Ser Val Trp Val Lys Gln
 510 515

aaaattactt tcctacatgc agagctttcc gatcactcat acaccaata taaattggaa 1772
 gctt 1776

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His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His Leu
 35 40 45

Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn
 50 55 60

Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys
 65 70 75 80

Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp

85

90

95

Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
 100 105 110

Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly Ile
 115 120 125

Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp Gly
 130 135 140

Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn Gln
 145 150 155 160

Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp Phe
 165 170 175

Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr His
 180 185 190

Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys Ile
 195 200 205

Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Ile
 210 215 220

Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met Asp
 225 230 235 240

His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr Thr
 245 250 255

Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His Ile
 260 265 270

Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr Thr
 275 280 285

Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu Ala
 290 295 300

Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val Phe
 305 310 315 320

Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly Gly
 325 330 335

Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys His

25

340	345	350
Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro Gly		
355	360	365
Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala Tyr		
370	375	380
Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr Gly		
385	390	395 400
Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser Lys		
405	410	415
Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr Gln		
420	425	430
His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu Gly		
435	440	445
Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp Gly		
450	455	460
Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly Gln		
465	470	475 480
Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile Asn		
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Trp Val Lys Gln		
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aagcttccaa tttatattgg gtgtat

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